==========

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=13; hr=14; min=24; sec=41; ms=226;]

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****

Reviewer Comments:

Seq Id 19 through 23

Invalid response for <213>, It can be either Artificial, Unknown or Genus species.

Please check for the similar errors in subsequent sequences.

****

Validated By CRFValidator v 1.0.3

Application No: 10511384 Version No: 2.0

Input Set:

Output Set:

Started: 2007-11-28 14:28:36.627
Finished: 2007-11-28 14:28:41.238
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 611 ms
Total Warnings: 229
Total Errors: 0
No. of SeqIDs Defined: 229
Actual SeqID Count: 229

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-11-28 14:28:36.627
Finished: 2007-11-28 14:28:41.238
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 611 ms
Total Warnings: 229
Total Errors: 0
No. of SeqIDs Defined: 229
Actual SeqID Count: 229

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (23)
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W 402	Undefined organism found in <213> in SEQ ID (25)
W 402	Undefined organism found in <213> in SEQ ID (26)
W 402	Undefined organism found in <213> in SEQ ID (27)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)

This error has occured more than 20 times, will not be displayed

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<140> 10511384
<141> 2007-11-28

<150> CU 2002/0076
<151> 2002-04-15

<150> EP98001000
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<210> 19
<211> 408
<212> PRT
<213> VEGF121 Isoform

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Thr Arg Pro Val Ala Leu His Ile Ser Thr Arg Pro Ser Glu Arg Leu
20 25 30

Glu Ala Leu Ala Leu Glu Leu Glu Leu Glu Thr Tyr Arg Leu Glu His
35 40 45

Ile Ser His Ile Ser Ala Leu Ala Leu Tyr Ser Thr Arg Pro Ser Glu
50 55 60

Arg Gly Leu Asn Ala Leu Ala Ala Leu Ala Pro Arg Met Glu Thr Ala
65 70 75 80

Leu Ala Gly Leu Gly Leu Tyr Gly Leu Tyr Gly Leu Tyr Gly Leu Asn
85 90 95

Ala Ser Asn His Ile Ser His Ile Ser Gly Leu Val Ala Leu Val Ala
100 105 110

Leu Leu Tyr Ser Pro His Glu Met Glu Thr Ala Ser Pro Val Ala Leu
115 120 125

Thr Tyr Arg Gly Leu Asn Ala Arg Gly Ser Glu Arg Thr Tyr Arg Cys
130 135 140

Tyr Ser His Ile Ser Pro Arg Ile Leu Glu Gly Leu Thr His Arg Leu
145 150 155 160

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Glu Val Ala Leu Ala Ser Pro Ile Leu Glu Pro His Glu Gly Leu Asn
                165                 170                 175

Gly Leu Thr Tyr Arg Pro Arg Ala Ser Pro Gly Leu Ile Leu Glu Gly
            180                 185                 190

Leu Thr Tyr Arg Ile Leu Glu Pro His Glu Leu Tyr Ser Pro Arg Ser
        195                 200                 205

Glu Arg Cys Tyr Ser Val Ala Leu Pro Arg Leu Glu Met Glu Thr Ala
    210                 215                 220

Arg Gly Cys Tyr Ser Gly Leu Tyr Gly Leu Tyr Cys Tyr Ser Cys Tyr
225                 230                 235                 240

Ser Ala Ser Asn Ala Ser Pro Gly Leu Gly Leu Tyr Leu Glu Gly Leu
                245                 250                 255

Cys Tyr Ser Val Ala Leu Pro Arg Thr His Arg Gly Leu Gly Leu Ser
            260                 265                 270

Glu Arg Ala Ser Asn Ile Leu Glu Thr His Arg Met Glu Thr Gly Leu
        275                 280                 285

Asn Ile Leu Glu Met Glu Thr Ala Arg Gly Ile Leu Glu Leu Tyr Ser
    290                 295                 300

Pro Arg His Ile Ser Gly Leu Asn Gly Leu Tyr Gly Leu Asn His Ile
305                 310                 315                 320

Ser Ile Leu Glu Gly Leu Tyr Gly Leu Met Glu Thr Ser Glu Arg Pro
                325                 330                 335

His Glu Leu Glu Gly Leu Asn His Ile Ser Ala Ser Asn Leu Tyr Ser
            340                 345                 350

Cys Tyr Ser Gly Leu Cys Tyr Ser Ala Arg Gly Pro Arg Leu Tyr Ser
        355                 360                 365

Leu Tyr Ser Ala Ser Pro Ala Arg Gly Ala Leu Ala Ala Arg Gly Gly
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Leu Asn Gly Leu Leu Tyr Ser Cys Tyr Ser Ala Ser Pro Leu Tyr Ser
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Pro Arg Ala Arg Gly Ala Arg Gly
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<213> VEGF121 Isoform

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gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180

atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240

atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300

aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360

agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420

aaatgtgaca agccgaggcg gtga 444

<210> 21
<211> 408
<212> PRT
<213> VEGF mutated isoform

<400> 21

Met Glu Thr Ala Ser Asn Pro His Glu Leu Glu Leu Glu Ser Glu Arg
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Thr Arg Pro Val Ala Leu His Ile Ser Thr Arg Pro Ser Glu Arg Leu
20 25 30

Glu Ala Leu Ala Leu Glu Leu Glu Leu Glu Thr Tyr Arg Leu Glu His
35 40 45

Ile Ser His Ile Ser Ala Leu Ala Leu Tyr Ser Thr Arg Pro Ser Glu
50 55 60

Arg Gly Leu Asn Ala Leu Ala Ala Leu Ala Pro Arg Met Glu Thr Ala
65 70 75 80

```
Leu Ala Gly Leu Gly Leu Tyr Gly Leu Tyr Gly Leu Tyr Gly Leu Asn
                85                  90                  95

Ala Ser Asn His Ile Ser His Ile Ser Gly Leu Val Ala Leu Val Ala
            100                 105                 110

Leu Leu Tyr Ser Pro His Glu Met Glu Thr Ala Ser Pro Val Ala Leu
        115                 120                 125

Thr Tyr Arg Gly Leu Asn Ala Arg Gly Ser Glu Arg Thr Tyr Arg Cys
    130                 135                 140

Tyr Ser His Ile Ser Pro Arg Ile Leu Glu Gly Leu Thr His Arg Leu
145                 150                 155                 160

Glu Val Ala Leu Ala Ser Pro Ile Leu Glu Pro His Glu Gly Leu Asn
                165                 170                 175

Gly Leu Thr Tyr Arg Pro Arg Ala Ser Pro Gly Leu Ile Leu Glu Gly
            180                 185                 190

Leu Thr Tyr Arg Ile Leu Glu Pro His Glu Leu Tyr Ser Pro Arg Ser
        195                 200                 205

Glu Arg Cys Tyr Ser Val Ala Leu Pro Arg Leu Glu Met Glu Thr Ala
    210                 215                 220

Arg Gly Cys Tyr Ser Gly Leu Tyr Gly Leu Tyr Cys Tyr Ser Cys Tyr
225                 230                 235                 240

Ser Ala Ser Asn Ala Ser Pro Gly Leu Gly Leu Tyr Leu Glu Gly Leu
                245                 250                 255

Cys Tyr Ser Val Ala Leu Pro Arg Thr His Arg Gly Leu Gly Leu Ser
            260                 265                 270

Glu Arg Ala Ser Asn Ile Leu Glu Thr His Arg Met Glu Thr Gly Leu
        275                 280                 285

Asn Ile Leu Glu Met Glu Thr Ala Leu Ala Ile Leu Glu Ala Leu Ala
    290                 295                 300

Pro Arg Ala Leu Ala Gly Leu Asn Gly Leu Tyr Gly Leu Asn His Ile
```

305 310 315 320

Ser Ile Leu Glu Gly Leu Tyr Gly Leu Met Glu Thr Ser Glu Arg Pro
325 330 335

His Glu Leu Glu Gly Leu Asn His Ile Ser Ala Ser Asn Leu Tyr Ser
340 345 350

Cys Tyr Ser Gly Leu Cys Tyr Ser Ala Arg Gly Pro Arg Leu Tyr Ser
355 360 365

Leu Tyr Ser Ala Ser Pro Ala Arg Gly Ala Leu Ala Ala Arg Gly Gly
370 375 380

Leu Asn Gly Leu Leu Tyr Ser Cys Tyr Ser Ala Ser Pro Leu Tyr Ser
385 390 395 400

Pro Arg Ala Arg Gly Ala Arg Gly
405

<210> 22
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<213> VEGF mutated isoform

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gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180

atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240

atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300

aacatcacca tgcagattat ggcaatcgca cctgcacaag gccagcacat aggagagatg 360

agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420

aaatgtgaca agccgaggcg gtaa 444

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<212> PRT
<213> KDR 1-3 fragments

<400> 23

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Leu Glu Ala Leu Ala Val Ala Leu Ala Leu Ala Leu Glu Thr Arg Pro
            20                  25                  30

Leu Glu Cys Tyr Ser Val Ala Leu Gly Leu Thr His Arg Ala Arg Gly
        35                  40                  45

Ala Leu Ala Ala Leu Ala Ser Glu Arg Val Ala Leu Gly Leu Tyr Leu
    50                  55                  60

Glu Pro Arg Ser Glu Arg Val Ala Leu Ser Glu Arg Leu Glu Ala Ser
65                  70                  75                  80

Pro Leu Glu Pro Arg Ala Arg Gly Leu Glu Ser Glu Arg Ile Leu Glu
                85                  90                  95

Gly Leu Asn Leu Tyr Ser Ala Ser Pro Ile Leu Glu Leu Glu Thr His
            100                 105                 110

Arg Ile Leu Glu Leu Tyr Ser Ala Leu Ala Ala Ser Asn Thr His Arg
        115                 120                 125

Thr His Arg Leu Glu Gly Leu Asn Ile Leu Glu Thr His Arg Cys Tyr
    130                 135                 140

Ser Ala Arg Gly Gly Leu Tyr Gly Leu Asn Ala Arg Gly Ala Ser Pro
145                 150                 155                 160

Leu Glu Ala Ser Pro Thr Arg Pro Leu Glu Thr Arg Pro Pro Arg Ala
                165                 170                 175

Ser Asn Ala Ser Asn Gly Leu Asn Ser Glu Arg Gly Leu Tyr Ser Glu
            180                 185                 190

Arg Gly Leu Gly Leu Asn Ala Arg Gly Val Ala Leu Gly Leu Val Ala
        195                 200                 205

Leu Thr His Arg Gly Leu Cys Tyr Ser Ser Glu Arg Ala Ser Pro Gly
    210                 215                 220

Leu Tyr Leu Glu Pro His Glu Cys Tyr Ser Leu Tyr Ser Thr His Arg
```

```
225                 230                 235                 240

Leu Glu Thr His Arg Ile Leu Glu Pro Arg Leu Tyr Ser Val Ala Leu
                245                 250                 255

Ile Leu Glu Gly Leu Tyr Ala Ser Asn Ala Ser Pro Thr His Arg Gly
            260                 265                 270

Leu Tyr Ala Leu Ala Thr Tyr Arg Leu Tyr Ser Cys Tyr Ser Pro His
        275                 280                 285

Glu Thr Tyr Arg Ala Arg Gly Gly Leu Thr His Arg Ala Ser Pro Leu
    290                 295                 300

Glu Ala Leu Ala Ser Glu Arg Val Ala Leu Ile Leu Glu Thr Tyr Arg
305                 310                 315                 320

Val Ala Leu Thr Tyr Arg Val Ala Leu Gly Leu Asn Ala Ser Pro Thr
                325                 330                 335

Tyr Arg Ala Arg Gly Ser Glu Arg Pro Arg Pro His Glu Ile Leu Glu
            340                 345                 350

Ala Leu Ala Ser Glu Arg Val Ala Leu Ser Glu Arg Ala Ser Pro Gly
        355                 360                 365

Leu Asn His Ile Ser Gly Leu Tyr Val Ala Leu Val Ala Leu Thr Tyr
    370                 375                 380

Arg Ile Leu Glu Thr His Arg Gly Leu Ala Ser Asn Leu Tyr Ser Ala
385                 390                 395                 400

Ser Asn Leu Tyr Ser Thr His Arg Val Ala Leu Val Ala Leu Ile Leu
                405                 410                 415

Glu Pro Arg Cys Tyr Ser Leu Glu Gly Leu Tyr Ser Glu Arg Ile Leu
            420                 425                 430

Glu Ser Glu Arg Ala Ser Asn Leu Glu Ala Ser Asn Val Ala Leu Ser
        435                 440                 445

Glu Arg Leu Glu Cys Tyr Ser Ala Leu Ala Ala Arg Gly Thr Tyr Arg
    450                 455                 460
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Pro Arg Gly Leu Leu Tyr Ser Ala Arg Gly Pro His Glu Val Ala Leu
465                 470                 475                 480

Pro Arg Ala Ser Pro Gly Leu Tyr Ala Ser Asn Ala Arg Gly Ile Leu
                485                 490                 495

Glu Ser Glu Arg Thr Arg Pro Ala Ser Pro Ser Glu Arg Leu Tyr Ser
            500                 505                 510

Leu Tyr Ser Gly Leu Tyr Pro His Glu Thr His Arg Ile Leu Glu Pro
        515                 520                 525

Arg Ser Glu Arg Thr Tyr Arg Met Glu Thr Ile Leu Glu Ser Glu Arg
    530                 535                 540

Thr Tyr Arg Ala Leu Ala Gly Leu Tyr Met Glu Thr Val Ala Leu Pro
545                 550                 555                 560

His Glu Cys Tyr Ser Gly Leu Ala Leu Ala Leu Tyr Ser Ile Leu Glu
                565                 570                 575

Ala Ser Asn Ala Ser Pro Gly Leu Ser Glu Arg Thr Tyr Arg Gly Leu
            580                 585                 590

Asn Ser Glu Arg Ile Leu Glu Met Glu Thr Thr Tyr Arg Ile Leu Glu
        595                 600                 605

Val Ala Leu Val Ala Leu Val Ala Leu Val Ala Leu Gly Leu Tyr Thr
    610                 615                 620

Tyr Arg Ala Arg Gly Ile Leu Glu Thr Tyr Arg Ala Ser Pro Val Ala
625                 630                 635                 640

Leu Val Ala Leu Leu Glu Ser Glu Arg Pro Arg Ser Glu Arg His Ile
                645                 650                 655

Ser Gly Leu Tyr Ile Leu Glu Gly Leu Leu Glu Ser Glu Arg Val Ala
            660                 665                 670
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